

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 29,76,000

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) \_\_\_\_ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/676,053  
 DATE: 10/10/2000  
 TIME: 16:09:17

Input Set : A:\17044 DIV SEQLIST.txt  
 Output Set : N:\CRF3\10102000\I676053.raw

Does Not Comply  
 Corrected Diskette Needed

See pp. 1, 2, 3

1 110 APPLICANT: Dolly, James Oliver  
 2 Ask, Peter Eel  
 3 Whoolan, Larry Allen  
 4 Smith, Michael Elwood  
 5 111 TITLE OF INVENTION: MODIFICATION OF CLOSTRIDIAL TOXINS FOR  
 6 USE AS TRANSPORT PROTEINS  
 7 112 FILE REFERENCE: 17044DIV  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/676,053  
 C--> 15 <141> CURRENT FILING DATE: 2000-09-28  
 17 113 PRICE APPLICATION NUMBER: 09/750,131  
 18 114 PRICE FILING DATE: 1997-05-01  
 19 115 PRICE APPLICATION NUMBER: PCT/GB/01293  
 20 116 PRICE FILING DATE: 1997-05-31  
 21 117 PRICE APPLICATION NUMBER: UK 9410871.9  
 22 118 PRICE FILING DATE: 1994-05-31  
 23 119 PRICE APPLICATION NUMBER: UK 9410871.1  
 24 120 PRICE FILING DATE: 1994-05-31  
 25 121 NUMBER OF SEQ ID NOS: 13  
 26 170 SOFTWARE: PASTAFY for Windows Version 3.0  
 27 210 SEQ ID NO: 1  
 28 211 LENGTH: 33  
 29 212 TYPE: DNA  
 30 213 ORGANISM: Artificial Sequence  
 W--> 36 <220> FEATURE:  
 W--> 36 <223> OTHER INFORMATION:  
 37 150 SEQUENCE:  
 38 taatagatgct agatagcat agactaaat aat  
 39 210 SEQ ID NO: 2  
 40 211 LENGTH: 33  
 41 212 TYPE: DNA  
 42 213 ORGANISM: Artificial Sequence  
 W--> 44 <220> FEATURE:  
 W--> 44 <223> OTHER INFORMATION:  
 45 150 SEQUENCE:  
 46 taatagatgct agatagcat agactaaat aat  
 47 210 SEQ ID NO: 3  
 48 211 LENGTH: 33  
 49 212 TYPE: DNA  
 50 213 ORGANISM: Artificial Sequence  
 W--> 52 <220> FEATURE:  
 W--> 52 <223> OTHER INFORMATION:  
 53 150 SEQUENCE:  
 54 taatagatgct agatagcat agactaaat aat  
 55 210 SEQ ID NO: 4  
 56 211 LENGTH: 33  
 57 212 TYPE: DNA  
 58 213 ORGANISM: Artificial Sequence

33

32

30

Many mistakes <220> <223>  
 too hard to explain the source  
 of the Artificial Sequence  
 See #12 in Error Summary  
 sheet.

RAW SEQUENCE LISTING  
 PATENT APPLICATION US/09/676,053

DATE: 10/10/2009  
 TIME: 16:00:10

Input Set: A:\17044 DIV SEQLIST.txt  
 Output Set: N:\CRF3\10102000\I676053.raw

W--> 60 <220> FEATURE:  
 W--> 60 <223> OTHER INFORMATION:  
 60 <400> SEQUENCE:  
 61 ttatcagatg actacatggg  
 63 <210> SEQ ID NO: 1  
 64 <211> LENGTH: 22  
 65 <212> TYPE: DNA  
 66 <213> ORGANISM: Artificial Sequence  
 W--> 68 <220> FEATURE:  
 W--> 68 <223> OTHER INFORMATION:  
 68 <400> SEQUENCE:  
 69 aadagcccttt ttttautaaa caa  
 71 <210> SEQ ID NO: 2  
 72 <211> LENGTH: 20  
 73 <212> TYPE: DNA  
 74 <213> ORGANISM: Artificial Sequence  
 W--> 76 <220> FEATURE:  
 W--> 76 <223> OTHER INFORMATION:  
 76 <400> SEQUENCE:  
 77 ggaattcttta ctatgatat cttaa  
 79 <210> SEQ ID NO: 3  
 80 <211> LENGTH: 19  
 81 <212> TYPE: DNA  
 82 <213> ORGANISM: Artificial Sequence  
 W--> 84 <220> FEATURE:  
 W--> 84 <223> OTHER INFORMATION:  
 84 <400> SEQUENCE:  
 85 gacacutgagc ttatgaa  
 87 <210> SEQ ID NO: 4  
 88 <211> LENGTH: 18  
 89 <212> TYPE: DNA  
 90 <213> ORGANISM: Artificial Sequence  
 W--> 92 <220> FEATURE:  
 W--> 92 <223> OTHER INFORMATION:  
 92 <400> SEQUENCE:  
 93 atgtataagt taatgagc  
 95 <210> SEQ ID NO: 5  
 96 <211> LENGTH: 18  
 97 <212> TYPE: DNA  
 98 <213> ORGANISM: Artificial Sequence  
 W--> 100 <220> FEATURE:  
 W--> 100 <223> OTHER INFORMATION:  
 100 <400> SEQUENCE:  
 101 caatttatata tgcaggac  
 103 <210> SEQ ID NO: 6  
 104 <211> LENGTH: 16  
 105 <212> TYPE: DNA  
 106 <213> ORGANISM: Artificial Sequence  
 W--> 108 <220> FEATURE:

*refer  
to  
p. 1*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/676,053

DATE: 10/10/2008  
TIME: 16:05:19

Input Set : A:\17044 DIV SEQLIST.txt  
Output Set: N:\CRF3\10102000\1676053.raw

W--> 108 <223> OTHER INFORMATION:  
108 <100> SEQUENCE: 10  
109 gtcacagcata tataaatt  
110 <210> SEQ ID NO: 11  
111 <211> LENGTH: 13  
112 <212> TYPE: PRT  
113 <213> ORGANISM: Unknown  
W--> 116 <220> FEATURE:  
W--> 116 <223> OTHER INFORMATION:  
116 <100> SEQUENCE: 11  
117 Cys Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly  
118 1 5 10  
119 <210> SEQ ID NO: 12  
120 <211> LENGTH: 29  
121 <212> TYPE: DNA  
122 <213> ORGANISM: Artificial Sequence  
W--> 125 <220> FEATURE:  
W--> 125 <223> OTHER INFORMATION:  
125 <100> SEQUENCE: 12  
126 atttcacccaa taaccataaa taattttag  
127 <210> SEQ ID NO: 13  
128 <211> LENGTH: 36  
129 <212> TYPE: DNA  
130 <213> ORGANISM: Artificial Sequence  
W--> 133 <220> FEATURE:  
W--> 133 <223> OTHER INFORMATION:  
133 <100> SEQUENCE: 13  
134 cgggatactt ctatatcatt gtaaat  
W--> 135 17044DIV PATENT  
W--> 136 Serial No. Not yet assigned  
111

*refer to  
P. 1*

*↓  
Extraneous material at end of  
file must be deleted. It is  
causing invalid count errors in  
sequence # 13*

## VERIFICATION SUMMARY

PATENT APPLICATION US/09/676,053

DATE: 10/10/2000

TIME: 10:00:00

Input Set: A:\17044 DIV SEQLIST.txt

Output Set: N:\CRF3\10102000\I676053.raw

L:15 M:258 C: Current Application Number differs. Replaced Current Application No  
L:16 M:258 W: Current Filing Date differs. Replaced Current Filing Date  
L:36 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:36 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:44 M:258 W: Mandatory Feature missing. -240- FEATURE:  
L:44 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:50 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:52 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:55 M:258 W: Mandatory Feature missing. -240- FEATURE:  
L:55 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:58 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:58 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:70 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:70 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:84 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:84 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:92 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:92 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:100 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:100 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:108 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:108 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:116 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:116 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:125 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:125 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:133 M:258 W: Mandatory Feature missing. -220- FEATURE:  
L:133 M:258 W: Mandatory Feature missing. -223- OTHER INFORMATION:  
L:135 M:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:2  
L:136 M:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:13  
L:136 M:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4